

Priebe  
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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/416,267

1632  
#6  
DATE: 02/10/2000  
TIME: 17:59:22

INPUT SET: S34718.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

SEQUENCE LISTING

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- (1) General Information:
  - (i) APPLICANT: LI, YI  
SU, KUI  
LI, HAODONG
  - (ii) TITLE OF INVENTION: HUMAN CYTOKINE POLYPEPTIDE
  - (iii) NUMBER OF SEQUENCES: 9
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE: Human Genome Sciences, Inc.
    - (B) STREET: 9410 Key West Avenue
    - (C) CITY: Rockville
    - (D) STATE: MD
    - (E) COUNTRY: USA
    - (F) ZIP: 20850
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER: 09/416,267
    - (B) FILING DATE: OCT-12-1999
    - (C) CLASSIFICATION:
  - (viii) ATTORNEY/AGENT INFORMATION:
    - (A) NAME: Joseph J. Kenny
    - (B) REGISTRATION NUMBER: 43,710
    - (C) REFERENCE/DOCKET NUMBER: PF270P1
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: 301-309-8504
    - (B) TELEFAX: 301-309-8439
- (2) INFORMATION FOR SEQ ID NO:1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 780 base pairs
    - (B) TYPE: nucleic acid

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47      (C) STRANDEDNESS: single
48      (D) TOPOLOGY: linear
49
50      (ii) MOLECULE TYPE: DNA (genomic)
51
52
53      (ix) FEATURE:
54          (A) NAME/KEY: sig_peptide
55          (B) LOCATION: 72..131
56
57      (ix) FEATURE:
58          (A) NAME/KEY: mat_peptide
59          (B) LOCATION: 132..740
60
61      (ix) FEATURE:
62          (A) NAME/KEY: CDS
63          (B) LOCATION: 72..740
64
65
66      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
67
68
69      GCACGAGGGC GACTTCGCGG GACCGTGGCG CATGTTTCCT GGGAGTTACT GATCATCTTC      60
70
71      TTTGAAGAAA C ATG AAG TTA CAC TAT GTT GCT GTG CTT ACT CTA GCC ATC      110
72          Met Lys Leu His Tyr Val Ala Val Leu Thr Leu Ala Ile
73          -20                      -15                      -10
74
75      CTG ATG TTC CTG ACA TGG CTT CCA GAA TCA CTG AGC TGT AAC AAA GCA      158
76      Leu Met Phe Leu Thr Trp Leu Pro Glu Ser Leu Ser Cys Asn Lys Ala
77          -5                      1                      5
78
79      CTC TGT GCT AGT GAT GTG AGC AAA TGC CTC ATT CAG GAG CTC TGC CAG      206
80      Leu Cys Ala Ser Asp Val Ser Lys Cys Leu Ile Gln Glu Leu Cys Gln
81      10                      15                      20                      25
82
83      TGC CGG CCG GGA GAA GGC AAT TGC TCC TGC TGT AAG GAG TGC ATG CTG      254
84      Cys Arg Pro Gly Glu Gly Asn Cys Ser Cys Cys Lys Glu Cys Met Leu
85          30                      35                      40
86
87      TGT CTT GGG GCC CTT TGG GAC GAG TGC TGT GAC TGT GTT GGT ATG TGT      302
88      Cys Leu Gly Ala Leu Trp Asp Glu Cys Cys Asp Cys Val Gly Met Cys
89          45                      50                      55
90
91      AAT CCT CGA AAT TAT AGT GAC ACA CCT CCA ACT TCA AAG AGC ACA GTG      350
92      Asn Pro Arg Asn Tyr Ser Asp Thr Pro Pro Thr Ser Lys Ser Thr Val
93          60                      65                      70
94
95      GAG GAG CTG CAT GAA CCG ATC CCT TCT CTC TTC CGG GCA CTC ACA GAA      398
96      Glu Glu Leu His Glu Pro Ile Pro Ser Leu Phe Arg Ala Leu Thr Glu
97          75                      80                      85
98
99      GGA GAT ACT CAG TTG AAT TGG AAC ATC GTT TCT TTC CCT GTT GCA GAA      446
  
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100 Gly Asp Thr Gln Leu Asn Trp Asn Ile Val Ser Phe Pro Val Ala Glu
101 90 95 100 105
102 494
103 GAA CTT TCA CAT CAT GAG AAT CTG GTT TCA TTT TTA GAA ACT GTG AAC
104 Glu Leu Ser His His Glu Asn Leu Val Ser Phe Leu Glu Thr Val Asn
105 110 115 120
106 542
107 CAG CCA CAC CAC CAG AAT GTG TCT GTC CCC AGC AAT AAT GTT CAC GCG
108 Gln Pro His His Gln Asn Val Ser Val Pro Ser Asn Asn Val His Ala
109 125 130 135
110 590
111 CCT TAT TCC AGT GAC AAA GAA CAC ATG TGT ACT GTG GTT TAT TTT GAT
112 Pro Tyr Ser Ser Asp Lys Glu His Met Cys Thr Val Val Tyr Phe Asp
113 140 145 150
114 638
115 GAC TGC ATG TCC ATA CAT CAG TGT AAA ATA TCC TGT GAG TCC ATG GGA
116 Asp Cys Met Ser Ile His Gln Cys Lys Ile Ser Cys Glu Ser Met Gly
117 155 160 165
118 686
119 GCA TCC AAA TAT CGC TGG TTT CAT AAT GCC TGC TGC GAG TGC ATT GGT
120 Ala Ser Lys Tyr Arg Trp Phe His Asn Ala Cys Cys Glu Cys Ile Gly
121 170 175 180 185
122 734
123 CCA GAA TGT ATT GAC TAT GGT AGT AAA ACT GTC AAA TGT ATG AAC TGC
124 Pro Glu Cys Ile Asp Tyr Gly Ser Lys Thr Val Lys Cys Met Asn Cys
125 190 195 200
126 780
127 ATG TTT TAAAGAAGAC AAATGCAAAC CAAAGCAACT TAGTAAAATA
128 Met Phe
129
130
131
132 (2) INFORMATION FOR SEQ ID NO:2:
133
134 (i) SEQUENCE CHARACTERISTICS:
135 (A) LENGTH: 223 amino acids
136 (B) TYPE: amino acid
137 (D) TOPOLOGY: linear
138
139 (ii) MOLECULE TYPE: protein
140
141 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
142
143 Met Lys Leu His Tyr Val Ala Val Leu Thr Leu Ala Ile Leu Met Phe
144 -20 -15 -10 -5
145
146 Leu Thr Trp Leu Pro Glu Ser Leu Ser Cys Asn Lys Ala Leu Cys Ala
147 1 5 10
148
149 Ser Asp Val Ser Lys Cys Leu Ile Gln Glu Leu Cys Gln Cys Arg Pro
150 15 20 25
151
152 Gly Glu Gly Asn Cys Ser Cys Cys Lys Glu Cys Met Leu Cys Leu Gly

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153          30          35          40
154
155 Ala Leu Trp Asp Glu Cys Cys Asp Cys Val Gly Met Cys Asn Pro Arg
156 45          50          55          60
157
158 Asn Tyr Ser Asp Thr Pro Pro Thr Ser Lys Ser Thr Val Glu Glu Leu
159          65          70          75
160
161 His Glu Pro Ile Pro Ser Leu Phe Arg Ala Leu Thr Glu Gly Asp Thr
162          80          85          90
163
164 Gln Leu Asn Trp Asn Ile Val Ser Phe Pro Val Ala Glu Glu Leu Ser
165          95          100          105
166
167 His His Glu Asn Leu Val Ser Phe Leu Glu Thr Val Asn Gln Pro His
168          110          115          120
169
170 His Gln Asn Val Ser Val Pro Ser Asn Asn Val His Ala Pro Tyr Ser
171          125          130          135          140
172
173 Ser Asp Lys Glu His Met Cys Thr Val Val Tyr Phe Asp Asp Cys Met
174          145          150          155
175
176 Ser Ile His Gln Cys Lys Ile Ser Cys Glu Ser Met Gly Ala Ser Lys
177          160          165          170
178
179 Tyr Arg Trp Phe His Asn Ala Cys Cys Glu Cys Ile Gly Pro Glu Cys
180          175          180          185
181
182 Ile Asp Tyr Gly Ser Lys Thr Val Lys Cys Met Asn Cys Met Phe
183          190          195          200
184

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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTACGGATCC AGCTGTAACA AAGCACTCTG TG

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs

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206 (B) TYPE: nucleic acid  
207 (C) STRANDEDNESS: single  
208 (D) TOPOLOGY: linear  
209  
210 (ii) MOLECULE TYPE: other nucleic acid  
211  
212  
213  
214 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
215  
216 GTCAAGCTTT TAAAACATGC AGTTCATACA TTTGAC  
217  
218 (2) INFORMATION FOR SEQ ID NO:5:  
219  
220 (i) SEQUENCE CHARACTERISTICS:  
221 (A) LENGTH: 40 base pairs  
222 (B) TYPE: nucleic acid  
223 (C) STRANDEDNESS: single  
224 (D) TOPOLOGY: linear  
225  
226 (ii) MOLECULE TYPE: other nucleic acid  
227  
228  
229  
230  
231 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
232  
233 GATAGGATCC GCCATCATGA AGTTACACTA TGTGCTGTG  
234  
235 (2) INFORMATION FOR SEQ ID NO:6:  
236  
237 (i) SEQUENCE CHARACTERISTICS:  
238 (A) LENGTH: 37 base pairs  
239 (B) TYPE: nucleic acid  
240 (C) STRANDEDNESS: single  
241 (D) TOPOLOGY: linear  
242  
243 (ii) MOLECULE TYPE: other nucleic acid  
244  
245  
246  
247  
248 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
249  
250 GTCAGGTACC TTAAAACATG CAGTTCATAC ATTTGAC  
251  
252 (2) INFORMATION FOR SEQ ID NO:7:  
253  
254 (i) SEQUENCE CHARACTERISTICS:  
255 (A) LENGTH: 67 base pairs  
256 (B) TYPE: nucleic acid  
257 (C) STRANDEDNESS: single  
258

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/416,267**

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Error

Original Text